Sequence Listing

#5

<110> Goddard,Audrey
Godowski,Paul J.
Gurney,Austin L.
Watanabe,Colin K.
Wood,William I.

<120> NOVEL POLYPEPTIDES HAVING SEQUENCE SIMILARITY TO CYTOKINE RECEPTORS AND NUCLEIC ACIDS ENCODING THE SAME

<130> P3121R1

<140> US 09/964,994
<141> 2001-09-26

<150> PCT/US00/08439
<151> 2000-03-30

<150> PCT/US01/06520
<151> 2001-02-28

<150> US 60/191,015
<151> 2000-03-21

<150> US 09/941,992
<151> 2001-08-28

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<212> DNA
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accaaaagga agacagcatc tgtttcctct ttggtcctga gctggttaaa 200

aggaacactg gttgcctgaa cagtcacact tgcaaccatg atgcctaaac 250

attgctttct aggcttcctc atcagtttct tccttactgg tgtagcagga 300

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ccgaaatttt cacaacattt tgcaatggca gcctgggagg gcacttactg 400

gcaacagcag tgtctatttt gtgcagtaca aaatcatgtt ctcatgcagc 450

atgaaaagct ctcaccagaa gccaagtgga tgctggcagc acatttcttg 500

taacttccca ggctgcagaa cattggctaa atatggacag agacaatgga 550

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gctcacagag cggttgaaat tgaagctcta acaccacact ccagctactg 950

tgtagtggct gaaatatatc agcccatgtt agacagaaga agtcagagaa 1000

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				20				25						30	
Gln	Arg	Val	Gln	Phe	Gln	Ser	Arg	Asn	Phe	His	Asn	Ile	Leu	Gln	
				35				40						45	
Trp	Gln	Pro	Gly	Arg	Ala	Leu	Thr	Gly	Asn	Ser	Ser	Val	Tyr	Phe	
				50				55						60	
Val	Gln	Tyr	Lys	Ile	Met	Phe	Ser	Cys	Ser	Met	Lys	Ser	Ser	His	
				65				70						75	
Gln	Lys	Pro	Ser	Gly	Cys	Trp	Gln	His	Ile	Ser	Cys	Asn	Phe	Pro	
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Gly	Cys	Arg	Thr	Leu	Ala	Lys	Tyr	Gly	Gln	Arg	Gln	Trp	Lys	Asn	
				95				100						105	
Lys	Glu	Asp	Cys	Trp	Gly	Thr	Gln	Glu	Leu	Ser	Cys	Asp	Leu	Thr	
				110				115						120	
Ser	Glu	Thr	Ser	Asp	Ile	Gln	Glu	Pro	Tyr	Tyr	Gly	Arg	Val	Arg	
				125				130						135	
Ala	Ala	Ser	Ala	Gly	Ser	Tyr	Ser	Glu	Trp	Ser	Met	Thr	Pro	Arg	
				140				145						150	
Phe	Thr	Pro	Trp	Trp	Glu	Thr	Lys	Ile	Asp	Pro	Pro	Val	Met	Asn	
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Ile Thr Gln Val Asn Gly Ser Leu Leu Val Ile Leu His Ala Pro
170 175 180

Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn Val Ser Ile Glu
185 190 195

Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile Asn Asn Ser
200 205 210

Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg Ala Val
215 220 225

Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val Ala
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Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
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Glu Arg Cys Val Glu Ile Pro
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gaagaattga ggctgcttgg gaggaaggcc aggaggaaca cgagactgag 250

agatgaattt tcaacagagg ctgcaaagcc tgtggacttt agccagaccc 300

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gaaggtgcct ctggatgctg tgaagagtct acagagaaga ttcttgtatt 1100

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cttctttacc cctcacaatc cttgccacag tgtggggcag tggatgggtg 1250

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             20                  25                  30

Val Val Leu Pro Cys Leu Gly Phe Thr Leu Leu Leu Trp Ser Gln
             35                  40                  45

Val Ser Gly Ala Gln Gly Gln Glu Phe His Phe Gly Pro Cys Gln
             50                  55                  60

Val Lys Gly Val Val Pro Gln Lys Leu Trp Glu Ala Phe Trp Ala
             65                  70                  75

Val Lys Asp Thr Met Gln Ala Gln Asp Asn Ile Thr Ser Ala Arg
             80                  85                  90

Leu Leu Gln Gln Glu Val Leu Gln Asn Val Ser Asp Ala Glu Ser
             95                 100                 105

Cys Tyr Leu Val His Thr Leu Leu Glu Phe Tyr Leu Lys Thr Val
            110                 115                 120

Phe Lys Asn His His Asn Arg Thr Val Glu Val Arg Thr Leu Lys
            125                 130                 135

Ser Phe Ser Thr Leu Ala Asn Asn Phe Val Leu Ile Val Ser Gln
            140                 145                 150

Leu Gln Pro Ser Gln Glu Asn Glu Met Phe Ser Ile Arg Asp Ser
            155                 160                 165

Ala His Arg Arg Phe Leu Leu Phe Arg Arg Ala Phe Lys Gln Leu
            170                 175                 180

Asp Val Glu Ala Ala Leu Thr Lys Ala Leu Gly Glu Val Asp Ile
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Leu Leu Thr Trp Met Gln Lys Phe Tyr Lys Leu
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